

## **THE ANALYSIS OF THE CORRELATIONS AND REGRESSIONS BETWEEN SOME CHARACTERS ON A WHEAT ISOGENIC VARIETIES ASSORTMENT**

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**Abstract:** In the years 2012-2014 on Banu-Maracine DRS there were tested an assortment of 25 isogenic lines of wheat (*Triticum aestivum ssp. vulgare*), the analyzed characters being the number of seeds/spike, seeds weight/spike (g), no. of spikes/m<sup>2</sup>, weight of a thousand seeds (WTS) (g) and no. of emerged plants/m<sup>2</sup>. Based on recorded data and statistical processing of those, they were identified a numbers of links between these characters. Also available regression models were identified between some of the studied characters. Based on component analysis, no. of seeds/spike and seeds weight/spike are components that influence in excess of 88% variance analysis, a total of seven genotypes with positive scores for both factors.

**Key words:** Yield elements, forecasting regression model, principal component analysis

### **1. Introduction**

The spikeliest cultivated forms of wheat were essentially landraces selected by farmers from wild populations, presumably because of their superior yield and other characteristics, an spikely and clearly non-scientific form of plant breeding! However, domestication was also associated with the selection of genetic traits that separated them from their wild relatives [4].

The spread of wheat from its site of origin across the world has been elegantly described by Feldman [3]. The achievement of a genetic diversity by cultivating more genotypes with different reactions at the conditions of environment, with different precocity, constitutes the simplest way of reduction the fluctuation of the yield to plant crop [2].

Generally, the seeds are a good start for the future culture, if they have a high biological value, coming from improved genotypes with the genetic, physiological and morphological index of quality. From this point of view, a high mitotic activity is directly proportional to the genetic viability of the seed. Analysis of the mitotic activity and the mitotic division indexes can reveal the genotypic specificity and genetic diversity [1].

Regarding the phenomenon of dwarfing on wheat, genetic bases are determined by *Rht* genes type that is known to breeders for over 40 spikes and although it has been extensively used in wheat, this gene cannot be transferred on other cereals [6]. Worldwide, there are not yet fully known *Rht* genes effects that they have on the plant, but it seems that their actions are multiple, affecting more than plant height [7]. Varieties with high straw secure better sunlight, butt end to break under its own weight because of the fragility stem. Fertilization with nitrogen, vital in crop conditions on soils with low and very low fertility, cannot be applied in this situation, since the plants are breaking or semi-dwarf varieties have no longer problems regarding fertilization [5].

### **2. Material and method**

In the years 2012-2014 on Banu-Maracine DRS were tested an assortment consists of 25 isogenic lines of common wheat (*Triticum aestivum ssp. vulgare*), with the combination of *rht1* & *Rht8* genes, the analyzed characters being the number of seeds/spike, the seeds weight/spike (g), the no. of spikes/m<sup>2</sup>, the weight of a thousand seeds (WTS) (g) and the no. of emerged plants/m<sup>2</sup>. The links between characters were analyzed be using the correlations and the regressions.

The evolution of the studied characters was monitored using forecasting regression models based on linear or nonlinear regression using polynomial equations. Validity forecasting regression models was determined by using the coefficient of determination ( $R^2$ ), the available models having a coefficient of determination greater than 0.7. Regarding the interpretation of the correlation coefficient value, it was considered that when this is positive, the relationship between variables X and Y is "positive", namely an increase of X value character determines the overall growth of character Y.

When correlation coefficient value relationship between the two variables is "negative", an increase of X character generally has as a consequence a decrease of Y character. The interpretation of the correlation coefficient was applied according Colton (1974.). In our experiment there were consider that correlation which have a correlation coefficient value higher than  $\pm 0.7$ . The regression forecasting models were calculated using polynomial equations. The regression model is considered valid when was calculated a coefficient of determination greater than 0.7. The coefficient of determination was based on the correlation coefficient, which is equal to the square of the correlation coefficient.

### 3. Results and discussions

Regarding the analyzed yield elements in Table 1 there is presented the variation of main parameters calculated. Thus, regarding the average no. of seeds/spike, it had a value of 20.37 seeds/spike with a standard deviation of 2.94 seeds/spike, limits of variation between 14.55 and 25.25 seeds/spike and an amplitude variation of 10.7 seeds/spike (Table 1). Regarding the seeds weight/spike, the average was 0.876 g seeds/spike, with a standard deviation of 0.16 g seeds/spike, limits of variation between 0.61 and 1.28 seeds/spike and an amplitude variation of 0.67 g seeds/spike.

**Table 1: The variation of calculated parameters for the studied character**

Character Parameter	No of seeds/spike	Seeds weight/spike (g)	No. of spike/m <sup>2</sup>	WTS (g)	No. of emerged plants/m <sup>2</sup>
Average	20.37	0.876	565.12	44.63	335.36
Range	14.55- 25.25	0.61-1.28	387-664	40-49.2	229-410
Variation amplitude	10.7	0.67	277	9.2	181
Standard deviation	2.94	0.16	77.64	2.71	48.47
Variability coefficient	14.43	18.26	13.74	6.07	14.45

Regarding the no. of spikes/m<sup>2</sup>, the average was 565.12 spikes/m<sup>2</sup>, with a standard deviation of 77.64 spikes/m<sup>2</sup>, limits of variation between 387 and 664 spikes/m<sup>2</sup> and an amplitude of variation of 277 spikes/m<sup>2</sup>. Regarding the WTS, the average was 44.63 g, with a standard deviation of 2.71 g, limits of variation between 40 and 49.2 g and 9.2 g amplitude variation. In the case of no. of emerged plants/m<sup>2</sup>, the average was 335.36 emerged pl./m<sup>2</sup>, with a standard deviation of 48.47 emerged pl./m<sup>2</sup>, the variation range between 229 and 410 emerged pl./m<sup>2</sup> and a variation amplitude of 181 emerged pl./m<sup>2</sup>.

In the present study, regarding the study on correlations between the studied characters, these are shown in Table 2. Thus, we identified strong links between:

- The no. of seeds/spike and seeds weight/spike, the correlation coefficient being of 0.824.
- The no. of seeds/spike and WTS, the correlation coefficient being equal with -0.822.
- The seeds weight/spike and WTS, the correlation coefficient being of -0.745.
- The emerged plants/m<sup>2</sup> and no. of spikes/m<sup>2</sup>, the correlation coefficient being of 0.841.

**Table 2: The analysis of the correlation coefficients between the studied characters**

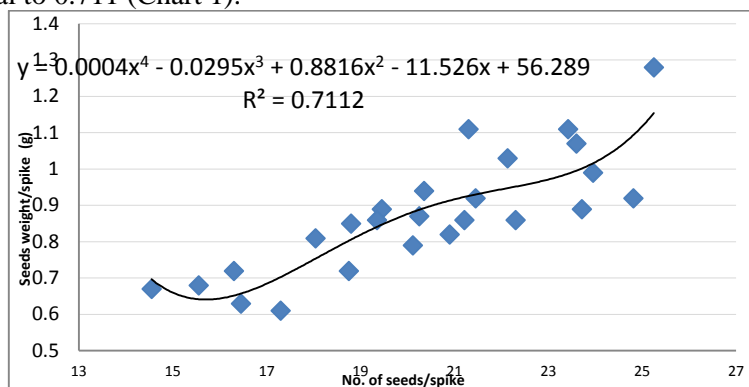
Character	No. of seeds/spike	Seeds weight/spike	No. of spike/m <sup>2</sup>	WTS
Seeds weight/spike	<b>0.824</b>	-	-	-
No. of spike/m <sup>2</sup>	0.037	0.057	-	-
WTS	<b>-0.822</b>	<b>-0.745</b>	-0.075	-
No. of emerged plants/m <sup>2</sup>	0.122	0.145	<b>0.841</b>	-0.096

From the analysis of the calculated correlation coefficients, the following predictions can be made regarding the biological mechanisms, as follows:

-Large negative value of the correlation coefficient between WTS and no. of seeds/spike, suggests that with increasing no. of seeds in the spike, their size of those decreases.

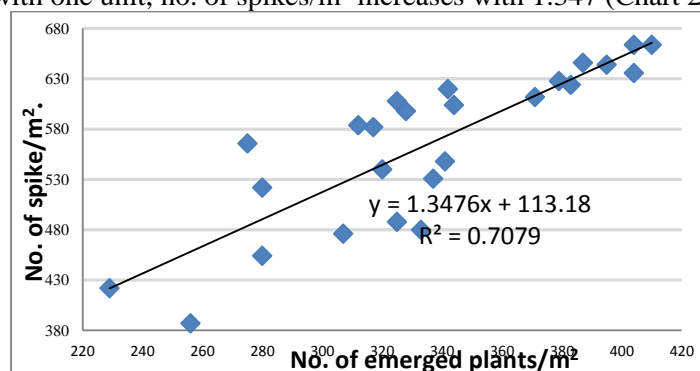
-The high value of the correlation coefficient between no. of seeds/spike and seeds weight/spike, naturally suggests that once the increase the no. of seeds in the spike, clearly and seeds weight increases too. In conclusion, when it grows no. of seeds/spike, decreasing their size of the seeds, but also increases the average weight of seeds produced by a spike, despite the decrease in seeds size. Concerning the regression analysis models available depending on the value of the correlation coefficient, in the case of regression model between the no. of seeds/spike and seeds

weight/spike, it was calculated a regression equation of degree 4 polynomial type, the coefficient of determination equal to 0.711 (Chart 1).



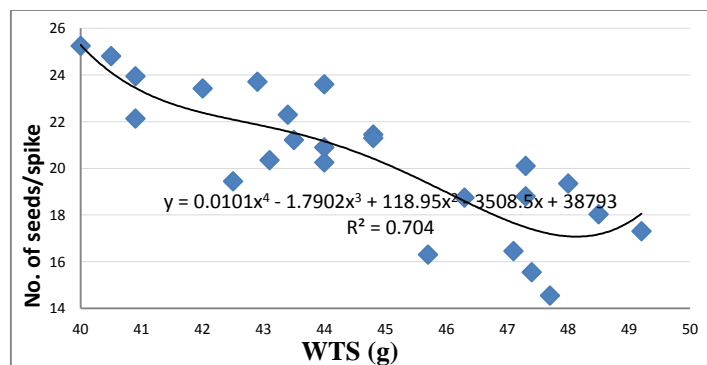
**Chart 1-The regression model analysis between no. of seeds/spike and seeds weight/spike**

Regarding the regression model analysis of emerged plants/m<sup>2</sup> and no. of spikes/m<sup>2</sup> it was calculated the linear regression equation, the coefficients of determination being equal with 0.7079, while the value of the regression coefficient was 1.347, which means that, when the no. of emerged plants/m<sup>2</sup> increases with one unit, no. of spikes/m<sup>2</sup> increases with 1.347 (Chart 2).



**Chart 2 - The regression model analysis between no. of emerged plants/m<sup>2</sup> and no. of spikes/m<sup>2</sup>**

Concerning the regression analysis models available depending on the value of the correlation coefficient, in the case of regression model between the no. of seeds/spike and WTS, it was calculated a regression equation of degree 4 polynomial type, the coefficient of determination was equal with 0.744 (Chart 3).



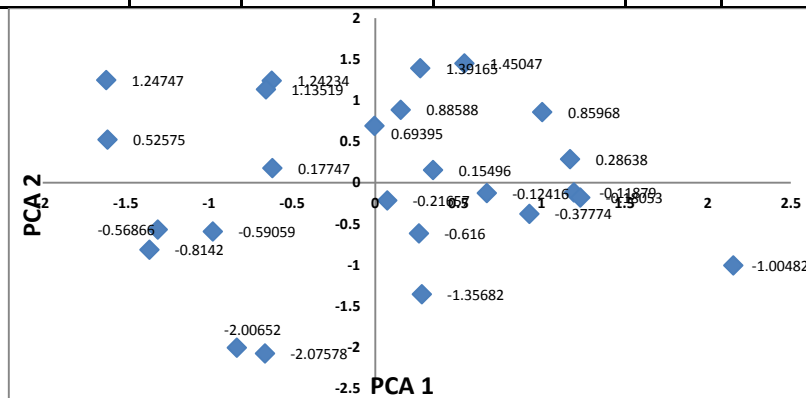
**Chart 3 - The regression model analysis between no. of seeds/spike and WTS**

In the present study it was carried out and principal components analysis (PCA). Thus the first two factors, namely no. of seeds/spike and seeds weight/spike influenced the variance to an extent of 88.78% (Table 3).

In this analysis, based on two components that scored the highest, there were identified the following groups (Chart 4): group I with seven genotypes, in which both components have positive scores; group II with eight genotypes, the first component has positive values and the second component is negative; group III genotypes having 5, where in both components have negative scores; group IV genotypes having 5, where the first component is negative and the second component is positive.

**Table 3: Eigenvalues and component score coefficients**

Component	Initial Eigenvalues			Component Score Coefficient Matrix	
	Total	% of Variance	Cumulative %	1	2
No. of seeds/spike	2.655	53.098	53.098	0.926	-0.214
Seeds weight/spike	1.784	35.686	88.784	0.903	-0.181
No. of spike/m <sup>2</sup>	0.266	5.317	94.100	0.261	0.924
WTS	0.163	3.251	97.351	-0.897	0.198
No. of emerged plants/m <sup>2</sup>	0.132	2.649	100.000	0.331	0.901



**Chart 4 - The chart of two main components, the no. of seeds/spike and the seeds weight/spike**

#### 4. Conclusions

Based on recorded data and statistical processing of it, it can draw the following conclusions:

1. Strong links were found between the no. of seeds/spike and seeds weight/spike, the no. of seeds/spike and WTS, the seeds weight/spike and WTS, the no. of emerged plants/m<sup>2</sup> and the no. of spikes/m<sup>2</sup>.
2. Based on the calculation of the coefficient of determination, the regression models were identified between the no. of seeds/spike and the seeds weight/spike, the no. of emerged plants/m<sup>2</sup> and the no. of spikes/m<sup>2</sup> and between the no. of emerged plants/m<sup>2</sup> and the no. of spikes/m<sup>2</sup>.
3. On the basis of the correlation coefficients values, we can deduce that when it increase the no. of seeds/spike, it decreases their size, but also increase the average weight of seeds produced by a spike, despite the decrease in seeds size.
4. Based on the analysis of components, no. of seeds/spike and seeds weight/spike are components that influence in excess of 88% variance analysis, a total of seven genotypes having positive scores for both factors.

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